

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 17:46:47 ; Search time 1892.13 Seconds
(without alignments)
16080.756 Million cell updates/sec

Title: US-10-018-786-7
Perfect score: 702
Sequence: 1 atgcgtcttgcaggatc.....cagtcaggatcttgctga 702

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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 - 4: gb_em:*
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- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A.,
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Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
Kitajima, J.P.
Comparison of the genomes of two Xanthomonas pathogens with
differing host specificities
Nature 417 (6887), 459-463 (2002)
2022145
PUBMED
12024217
2 (bases 1 to 11629)
da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
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Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
Kitajima, J.P.
Direct Submission
Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
Brazil

FEATURES
source

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CDS

gene

CDS

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Job time : 1897.13 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 17:42:57 ; Search time 205.168 Seconds
(without alignments)
14535.578 Million cell updates/sec

Title: US-10-018-786-7
Perfect score: 702
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0s
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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 AC ABL57895;
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 11-SEP-2003 (revised)
 DT 04-JUL-2002 (first entry)
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 DE Partial hypersensitive reaction and pathogenicity, hrpB5 gene.
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 KW Hypersensitive reaction and pathogenicity; hrpB5; exo-polysaccharide;
 KW xanthan gum; gene; ds.

XX Xanthomonas campestris; pv vesicatoria.
 OS WO200078967-A1.
 PN 28-DEC-2000.
 PD 21-JUN-2000; 2000WO-FR001725.
 PF 22-JUN-1999; 99FR-00007963.
 XX (RHOD) RHODIA CHIM.
 PA Pierrard J, Simon J, Chevallereau P;
 PI WPI; 2001-102725/11.
 XX New Xanthomonas campestris bacteria strains for use in production of exo-
 PT polysaccharides are made non-virulent by inactivation of at least one
 PT virulence gene.
 XX Claim 19; Page 27; 33pp; French.
 XX The present invention relates to new Xanthomonas campestris bacteria
 CC strains made non-virulent by inactivation of at least one virulence gene
 CC but which have retained the capacity to produce exo-polysaccharides
 CC (preferably xanthan gum). One such virulence gene deleted to produce the
 CC bacterial strains was the hrpB5 gene (Hypersensitive Reaction and
 CC pathogenicity). The hrp genes are essential for pathogenicity in plants.
 CC The present sequence is a partial sequence of the hrpB5, used in an
 CC example from the invention. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX Sequence 702 BP; 97 A; 233 C; 266 G; 106 T; 0 U; 0 Other;
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 Matches 702; Conservative 0; Mismatches 0;
 QY 1 ATGCGCTTTTGGCTGAGGTCACACCGAGCGGTGGCGCTTGACTGCGAGGTATCCCA 60
 DB 1 ATGCGCTTTTGGCTGAGGTCACACCGAGCGGTGGCGCTTGACTGCGAGGTATCCCA 60
 QY 61 CGCAGGCGATTTGGCTGTGCTGGAATGGAACGAGCGGGTGCACAGTGCACGGCGGT 120
 DB 61 CGCAGGCGATTTGGCTGTGCTGGAATGGAACGAGCGGGTGCACAGTGCACGGCGGT 120
 QY 121 TGGCGCGACGCGCTGGCGGACGCCACAGCGGTGCGCAGCGCTGCTCGACGCTGCCAA 180
 DB 121 TGGCGCGACGCGCTGGCGGACGCCACAGCGGTGCGCAGCGCTGCTCGACGCTGCCAA 180
 QY 181 CGGCAGGCGCGAGGCCATTCCTTCAAGATGCCACGACGAGGCGCGAGCGCATGCA 240
 DB 181 CGGCAGGCGCGAGGCCATTCCTTCAAGATGCCACGACGAGGCGCGAGCGCATGCA 240
 QY 241 GGCTATGGCGCGCGGCTGGCGCGTCACTGACGCGGTGGAACGAGCGCGGTGGCGCAT 300

241	DB	GGCTATGCGCGCGGCTGGCGCCGTCAAGCTCGACGCGCTGGAACGAGGCGCGGCGTGGGCGAT	300
301	QY	GCGTTCGGGCGCCAGGACGCGCGACGGCGCGCCGCGAGCGCTGGCCGAGATCGTCCGC	360
301	DB	GCGTTCGGGCGCCAGGACGCGCGACGGCGCGCCGCGAGCGCTGGCCGAGATCGTCCGC	360
361	QY	CAGCGCTGCGAGCAGGTTCTGCACGCGCAGCATCCTTCGCGCGCTGTACGCGCGCGCCGCA	420
361	DB	CAGCGCTGCGAGCAGGTTCTGCACGCGCAGCATCCTTCGCGCGCTGTACGCGCGCGCCGCA	420
421	QY	CAGGCGCTGGACGCGCGCTTGGACGAGGCGCAACGCGCTTCGAGGTGAGCTGATCCCGAT	480
421	DB	CAGGCGCTGGACGCGCGCTTGGACGAGGCGCAACGCGCTTCGAGGTGAGCTGATCCCGAT	480
481	QY	CGGCTGGACGATACGACGCGCGCGCTTCGATCGCGCGCGACAGCGCGCGGATGAGAGCATG	540
481	DB	CGGCTGGACGATACGACGCGCGCGCTTCGATCGCGCGCGACAGCGCGCGGATGAGAGCATG	540
541	QY	CGGCTGGAACATGTCCGCTGATACGACTCTGGCTTGGGTGCGCTGGCAATGGGAT	600
541	DB	CGGCTGGAACATGTCCGCTGATACGACTCTGGCTTGGGTGCGCTGGCAATGGGAT	600
601	QY	ACCGGCGGTGTTCCGACCGCAACTCGGTGATCAGGTGCGGAGTCTCCGGCGCGTCATTCGC	660
601	DB	ACCGGCGGTGTTCCGACCGCAACTCGGTGATCAGGTGCGGAGTCTCCGGCGCGTCATTCGC	660
661	QY	CGGCTGTTGGCCACCGCGACGCGCGGTCCGCGATGCTTCTGCA	702
661	DB	CGGCTGTTGGCCACCGCGACGCGCGGTCCGCGATGCTTCTGCA	702

COM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 20:18:17 ; Search time 1351.57 Seconds
(without alignments)

15510.269 Million cell updates/sec

Title: US-10-018-786-7

Perfect score: 702
Sequence: 1 atgcgtctttggctgaggtc.....cggtgccgagatcgttgctga 702

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 08

Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_estbun:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_huc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_ests3:*
13: gb_ests4:*
14: gb_est5:*
15: em_estfun:*
16: em_eston:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_red:*
26: em_gss_prg:*
27: em_gss_vrl:*

Search completed: July 7, 2004, 21:07:53
Job time : 209.168 secs

28: gb_gss1: +
 29: gb_gss2: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	83.4	11.9	935	CNS006XK	AL066051 Drosophil
c 2	83.3	11.8	1131	AG042920	AG042920 Pan trogl
c 3	81.6	11.6	1244	BGS46745	BGS46745 1024014H0
c 4	77.4	11.0	1201	BX340009	BX340009 BX340009
c 5	76.8	10.9	982	BX415111	BX415111 BX415111
c 6	75.4	10.9	925	CNS0091P	AL053013 Drosophil
c 7	75.4	10.7	1452	AG032979	AG032979 Pan trogl
c 8	74.2	10.6	925	CNS0091P	AL053013 Drosophil
c 9	73	10.4	1023	AG128304	AG128304 Pan trogl
c 10	72.6	10.3	1134	AG043044	AG043044 Pan trogl
c 11	72	10.3	893	AZ193531	AZ193531 SP_1023 B
c 12	71.8	10.2	1598	AG030579	AG030579 Pan trogl
c 13	71.2	10.1	1101	AG039543	AG039543 Pan trogl
c 14	71.2	10.1	1201	BX340009	BX340009 BX340009
c 15	71	10.1	1104	AG062490	AG062490 Pan trogl
c 16	70.8	10.1	932	CNS0072Q	AL066742 Drosophil
c 17	70.8	10.1	1610	BZ569386	BZ569386 pacs2-164
c 18	70.6	10.1	1189	AG030608	AG030608 Pan trogl
c 19	70.4	10.0	1421	BZ569488	AG030608 Pan trogl
c 20	70.2	10.0	1798	AG171124	BZ569488 pacs2-164
c 21	70	10.0	935	CNS006XK	AG171124 Pan trogl
c 22	70	10.0	1438	BZ557931	AL066051 Drosophil
c 23	70	10.0	1538	AG030607	BZ557931 pacs1-60
c 24	69.4	9.9	1432	AG032979	AG030607 Pan trogl
c 25	69.4	9.9	1626	AW731212	AG032979 Pan trogl
c 26	69.2	9.9	1026	BZ569417	AW731212 GA_Ea001
c 27	69.2	9.9	1299	AG039481	AG159205 Pan trogl
c 28	69.2	9.9	1348	CG752544	BZ569417 pacs2-164
c 29	69.2	9.9	1348	CG752544	AG039481 Pan trogl
c 30	68.8	9.8	1157	BM466479	CG752544 P047-2-C1
c 31	68.6	9.8	932	CNS0072Q	BM466479 AGENCOURT
c 32	68.6	9.8	1132	CK210297	AL066742 Drosophil
c 33	68.4	9.7	1037	CNS04060	CK210297 FGASQ2209
c 34	68.4	9.7	1083	CK206171	AL276477 Tetradon
c 35	68.2	9.7	1163	AG030649	CK206171 FGASQ1775
c 36	68.2	9.7	1201	BX405071	AG030649 Pan trogl
c 37	67.6	9.6	1387	AW731151	BX405071 BX405071
c 38	67.4	9.6	1542	AG032943	AW731151 GA_Ea001
c 39	67.2	9.6	1200	BX415896	AG032943 Pan trogl
c 40	67	9.5	1120	AG136785	BX415896 BX415896
c 41	66.6	9.5	842	AG058791	AG136785 Pan trogl
c 42	66.4	9.5	1124	AG041123	AG058791 Pan trogl
c 43	66.4	9.5	1232	AG072425	AG041123 Pan trogl
c 44	66.4	9.5	1273	BM562099	AG072425 Pan trogl
c 45	66.4	9.5	1277	AG060206	BM562099 AGENCOURT
c 46	66.4	9.5	1277	AG060206	AG060206 Pan trogl